

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/591,447DATE: 04/10/97
TIME: 08:30:46

INPUT SET: S16854.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: QUENTIN-MILLET, Marie-Jose et al.
6
7 (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN
8 RECEPTOR OF NEISSERIA MENINGITIDIS
9
10 (iii) NUMBER OF SEQUENCES: 42
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: LARSON AND TAYLOR
14 (B) STREET: 727 SOUTH 23RD STREET
15 (C) CITY: ARLINGTON
16 (D) STATE: VIRGINIA
17 (E) COUNTRY: USA
18 (F) ZIP: 22202
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/591,447
28 (B) FILING DATE: 29-JAN-1996
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: SARRO, THOMAS P
33 (B) REGISTRATION NUMBER: 19,196
34 (C) REFERENCE/DOCKET NUMBER: XI/P02956
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 703-920-7200
38 (B) TELEFAX: 703-892-8428
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 2230 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: DNA (genomic)
50
51 (vi) ORIGINAL SOURCE:
52 (A) ORGANISM: Neisseria meningitidis
53 (B) STRAIN: IM2169
54
55 (ix) FEATURE:
56 (A) NAME/KEY: sig_peptide
57 (B) LOCATION: 60..119
58
59 (ix) FEATURE:
60 (A) NAME/KEY: mat_peptide
61 (B) LOCATION: 120..2192
62
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 60..2192
66
67 (ix) FEATURE:
68 (A) NAME/KEY: misc_feature
69 (B) LOCATION: 120..1154
70
71 (ix) FEATURE:
72 (A) NAME/KEY: misc_feature
73 (B) LOCATION: 1155..1748
74
75 (ix) FEATURE:
76 (A) NAME/KEY: misc_feature
77 (B) LOCATION: 1749..2192
78
79 (ix) FEATURE:
80 (A) NAME/KEY: misc_binding
81 (B) LOCATION: 237..1169
82
83
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
85
86 ATTTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT 59
87
88 ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107
89 Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
90 -20 -15 -10 -5
91
92 TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155
93 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
94 1 5 10
95
96 GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203
97 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
98 15 20 25
99

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100	TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG	251
101	Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
102	30 35 40	
103		
104	ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG	299
105	Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu	
106	45 50 55 60	
107		
108		
109		
110	GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
111	Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
112	65 70 75	
113		
114	CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
115	Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
116	80 85 90	
117		
118	ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
119	Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
120	95 100 105	
121		
122	AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT	491
123	Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn	
124	110 115 120	
125		
126	CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT	539
127	Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe	
128	125 130 135 140	
129		
130	TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG	587
131	Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys	
132	145 150 155	
133		
134	TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA	635
135	Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg	
136	160 165 170	
137		
138	CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT	683
139	Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe	
140	175 180 185	
141		
142	GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT	731
143	Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro	
144	190 195 200	
145		
146	TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC	779
147	Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser	
148	205 210 215 220	
149		
150	GAA GAA TAT TCC AAG AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG	827
151	Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu	
152	225 230 235	

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206	Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr	
207	430 435 440	
208		
209	CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG	1499
210	Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly	
211	445 450 455 460	
212		
213	GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA	1547
214	Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys	
215	465 470 475	
216		
217		
218		
219		
220	ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC	1595
221	Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr	
222	480 485 490	
223		
224	GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA	1643
225	Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly	
226	495 500 505	
227		
228	AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG	1691
229	Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met	
230	510 515 520	
231		
232	TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA	1739
233	Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln	
234	525 530 535 540	
235		
236	AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA	1787
237	Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr	
238	545 550 555	
239		
240	AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA	1835
241	Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu	
242	560 565 570	
243		
244	TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT	1883
245	Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala	
246	575 580 585	
247		
248	GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC	1931
249	Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly	
250	590 595 600	
251		
252	AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC	1979
253	Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu	
254	605 610 615 620	
255		
256	GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC	2027
257	Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala	
258	625 630 635	

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SEQUENCE VERIFICATION REPORT
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Original Text